REVIEW 10.1111/j.1469-0691.2012.03816.x

Wild great apes as sentinels and sources of infectious disease

S. Calvignac-Spencer[1], S. A. J. Leendertz[1], T. R. Gillespie[2,3] and F. H. Leendertz[1]

1) *Emerging Zoonoses, Robert Koch-Institut, Berlin, Germany,* 2) *Department of Environmental Studies and Program in Population Biology, Ecology and Evolution, Emory University, Atlanta, GA and* 3) *Department of Environmental Health, Rollins School of Public Health, Emory University, Atlanta, GA, USA*

Abstract

Emerging zoonotic infectious diseases pose a serious threat to global health. This is especially true in relation to the great apes, whose close phylogenetic relationship with humans results in a high potential for microorganism exchange. In this review, we show how studies of the microorganisms of wild great apes can lead to the discovery of novel pathogens of importance for humans. We also illustrate how these primates, living in their natural habitats, can serve as sentinels for outbreaks of human disease in regions with a high likelihood of disease emergence. Greater sampling efforts and improvements in sample preservation and diagnostic capacity are rapidly improving our understanding of the diversity and distribution of microorganisms in wild great apes. Linking non-invasive diagnostic data with observational health data from great apes habituated to human presence is a promising approach for the discovery of pathogens of high relevance for humans.

Keywords: Chimpanzee, disease ecology, emerging infectious diseases, gorilla, zoonoses
Article published online: 22 February 2012
Clin Microbiol Infect 2012; **18:** 521–527

Corresponding author: F. H. Leendertz, Emerging Zoonoses, Robert Koch-Institut, Nordufer 20, 13353 Berlin, Germany
E-mail: leendertzf@rki.de

Introduction

Emerging infectious diseases frequently originate from zoonotic transmission events implicating wildlife reservoirs [1], with the highest risk for emergence being seen in tropical countries with high biodiversity and low infrastructure [2]. Consequently, the characterization of microorganisms infecting wildlife in the tropics is central to the development of global health surveillance systems that are capable of identifying putative pathogens before they enter the human population [1,2]. However, where should we start? Technically, it is possible to broadly screen various wildlife and vector species for known and unknown pathogens (e.g. viruses in mosquitoes [3], bats, or rodents [4]). But what does the identification of various (new) microorganisms tell us? Are they of pathogenic importance for humans? For some microorganisms, we may be able to assume zoonotic and pathogenic potential, owing to relatedness to known pathogens, but a true understanding of the risk associated with each microorganism requires comprehensive study of a large number of well-characterized samples from healthy and symptomatic humans from affected areas. This time-consuming and expensive process often yields results only after a pathogen has emerged from a wildlife source and become established in the human population. Fortunately, we can identify hosts with a high potential for carrying microorganisms of importance for humans, on the basis of host demography, ecology, and behaviour. Focusing on such high-potential hosts will improve our chances of understanding a microorganism with emergence potential well before it becomes established in humans [5]. Ideally, candidates should be high-density animal species exhibiting extensive niche overlap with humans in tropical regions, such as rodents or bats.

Another criterion for selecting target species is to focus on hosts with close evolutionary relatedness to humans. Close relatedness between species (including primates) has been shown to increase the likelihood of cross-species transmission events [5,6], and closely related species are also more likely to develop similar clinical signs when infected with specific pathogens [7].

Therefore, wild great apes are promising candidates for screening for potential new zoonotic agents. First, they are the closest evolutionary relatives of humans, facilitating microorganism transmission, which has, for example, led to the emergence of human immunodeficiency virus-1 [8]. Second, it has been shown that great apes suffer from acute and chronic diseases of high importance to humans, such as those caused by Ebola viruses and simian immunodeficiency viruses (SIVs), respectively [9,10], and can therefore serve as 'indicator species' for pathogens of clinical importance for humans. Third, there is intense exposure of humans to body fluids and tissues of great apes, as all non-human primate species are commonly hunted in West and Central Africa [11].

However, all great ape species are highly endangered, and invasive studies including anaesthesia or even euthanasia, such as those performed on bats on rodents, are ethically impossible [12]. The only invasive samples that it is ethically possible to collect are samples obtained from animals found dead (in bushmeat markets or in the wild) or samples collected in the course of interventions necessary to save the lives of great apes (e.g. hunting snare removal) [7]. In order to study microorganisms in living wild great apes, methods have been developed to allow the detection of microorganisms and antibodies in materials that can be collected non-invasively from these animals without disturbing them. Such investigations rely mostly on faeces, but in some cases also on urine or food wadges [7,13,14], and have led to the identification of at least 12 families and 17 genera of viruses infecting wild great apes (Table 1).

In this review, we summarize the current knowledge regarding the diversity of enzootic and non-enzootic microorganisms of African wild great apes (almost no information is available on microorganisms of Asian wild great apes), with a special emphasis on great apes as sentinels for emerging infectious diseases. We also highlight important gaps in our knowledge and areas in urgent need of further investigation. We did not consider data obtained from captive or semi-captive wild ape populations, which is not to say that they are uninformative, but rather that they are more likely to be biased [15]. Additionally, a comprehensive overview of this field of research would be beyond the scope of a review, so we have restricted our overview to the best-studied microorganisms at the ape–human interface.

Great Ape Enzootic Microorganisms

Most microorganisms identified in wild great apes appear to be enzootic (that is, they persistently infect wild great ape populations), and are not known to be associated with acute disease. This is nicely exemplified by viruses such as adenoviruses, hepadnaviruses, herpesviruses, parvoviruses, picornaviruses, polyomaviruses, and retroviruses (Table 1), and also applies to most gastrointestinal helminths, protozoa, and bacteria [7,16,17].

In contrast, nothing is known about enzootic pathogens spreading through populations and causing acute disease or death. For humans, various acute disease-causing endemic pathogens are known, e.g. smallpox or measles viruses. One may argue that this is simply because of a lack of surveillance in wild ape populations; however, habituated communities of wild great apes are distributed across each species range, and some of these communities have been under continuous observation for decades, so massive die-offs would not have gone unnoticed. A more likely explanation is that great ape demography (i.e. low-density, fragmented populations) is not compatible with the sustained circulation of such acute disease-causing pathogens. Known acute diseases in wild great apes originated either from other species (Ebola) [10], the environment (anthrax) [18], or humans (respiratory diseases) [19] (see below).

Great Ape Non-enzootic Microorganisms

A number of microorganisms infect wild great apes by environmental means, at least in the initial phases of what might later become an epizootic sustained by within-species transmission. Such infections occur through the consumption of contaminated food items, direct (e.g. biting) or indirect (e.g. aerosols) contact with other species, or vector bites (arthropods).

Microorganisms acquired though contaminated food

Obviously, all wild great apes are exposed to foodborne microorganisms, including other animal microorganisms found on vegetation as a consequence of contamination by infected animal fluids. Although diets typically exhibit significant variation at multiple scales (e.g. within subspecies or species, within regions, or over seasons for a specific population), the most striking differences are seen between the omnivorous genus *Pan* (chimpanzees and bonobo) and the herbivorous genus *Gorilla*. Chimpanzee and bonobo diets consist primarily of fruit and other plant parts, but animals, including other non-human primates, are eaten on occasion, with interesting regional differences in diet composition [20,21]. Thus, chimpanzees and bonobos are more likely to acquire microorganisms from other non-human primate species than are gorillas, which have never been observed to consume non-human primates or other animals in the wild [22,23].